



SEQUENCE LISTING

<110> Kato, Seishi
Sekine, Shingo
Kimura, Tomoko
Kobayashi, Midori

<120> HUMAN PROTEINS HAVING SECRETORY SIGNAL
SEQUENCES AND DNAs ENCODING THESE PROTEINS

<130> GIN-6/U40PUS

<140> US 09/254,760
<141> 1999-04-16

<150> JP 8/243,060
<151> 1996-09-13

<150> PCT/JP97/03239
<151> 1997-09-12

<160> 27

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 154
<212> PRT
<213> Homo sapiens

<400> 1

Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala
1 5 10 15
Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
20 25 30
Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
35 40 45
Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His
50 55 60
Arg Ser Arg Met Pro Lys Arg Ser Gly Ile Ile Val Thr Val Asp Ile
65 70 75
Leu Tyr Ser Val Arg Ile Ile Asn Lys Tyr Lys Ile Tyr His Ile Tyr Ile
80 85 90
Pro Pro Ser Val Cys Gin Pro Arg Gin Glu Met Gly Ser Gly Val His
100 105 110
Gin Leu Phe Gly Asp Glu Leu Gly Trp Arg Val Leu Glu Pro Glu Leu
115 120 125
Thr Gin Ile Cys Leu Phe Leu Leu Ala Ile Val Ile Ala Thr Val Ala
130 135 140

<400+2

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
1 5 10 15
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
20 25 30
Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
35 40 45
His Asp Ala Phe Leu Gly Ala Glu Ala Lys Thr Phe Asp Ala Leu
50 55 60
Ile Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
65 70 75 80
Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
85 90 95
Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
100 105 110
Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
115 120 125
Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
130 135 140
Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
145 150 155 160
Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
165 170 175
Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
180 185 190
Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
195 200 205
Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
210 215 220
Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
225 230 235 240
Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp
245 250 255
Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His
260 265 270
Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu
275 280 285 290
Gln Ile Val Asp Lys Tyr Asp Leu Ile Thr Val Asp Asn Lys Asp
295 300 305
Thr Asp Ile Asp Lys Asp Tyr Asp His Asp Asn Lys Asp
310 315 320

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<211+158

<212+158

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<211> 376
<212> ERT
<213> *Homo sapiens*

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 1 5 10 15
 Ala Val Pro Ile Asp Asp Pro Glu Asp Gly Gly Lys His Trp Val Val
 20 25 30
 Ile Val Ala Gly Ser Asn Gly Trp Tyr Asn Tyr Arg His Gln Ala Asp
 35 40 45
 Ala Cys His Ala Tyr Gln Ile Ile His Arg Asn Gly Ile Pro Asp Glu
 50 55 60
 Gln Ile Val Val Met Met Tyr Asp Asp Ile Ala Tyr Ser Glu Asp Asn
 65 70 75 80
 Pro Thr Pro Gly Ile Val Ile Asn Arg Pro Asn Gly Thr Asp Val Tyr
 85 90 95
 Gln Gly Val Pro Lys Asp Tyr Thr Gly Glu Asp Val Thr Pro Gln Asn
 100 105 110
 Phe Leu Ala Val Leu Arg Gly Asp Ala Glu Ala Val Lys Gly Ile Gly
 115 120 125
 Pro Gly Lys Val Ile Lys Ser Gly Pro Gln Asp Val Ile Phe Ile Tyr
 130 135 140
 Ile Ile Asp His Gly Ser Thr Gly Ile Ile Val Ile Asp Ile Asn Ile Asp
 145 150 155
 Ile His Ile Asp Asp Ile Asn Val Thr Ile His Asp Met Tyr Ile His
 160 165 170
 Lys Met Tyr Arg Lys Met Val Ile Tyr Ile Glu Ala Lys Glu Ser Gly
 180 185 190
 Ser Met Met Asn His Leu Pro Asp Asn Ile Asn Val Tyr Ala Thr Thr
 195 200 205
 Ala Ala Asn Ile Asp Asp Ile Asp Tyr Ala Tyr Tyr Tyr Asp Ile Asp
 210 215 220

Lys Ala Ser Ser Pro Val Pro Ileu Pro Pro Val Thr His Leu Asp Leu
 290 295 300
 Thr Pro Ser Pro Asp Val Pro Leu Thr Ile Met Lys Arg Lys Leu Met
 305 310 315 320
 Asn Thr Asn Asp Leu Glu Glu Ser Arg Gln Leu Thr Glu Glu Ile Gln
 325 330 335
 Arg His Leu Asp Tyr Glu Tyr Ala Leu Arg His Leu Tyr Val Leu Val
 340 345 350
 Asn Leu Cys Glu Lys Pro Tyr Ile Leu His Asn Ile Lys Leu Ser Met
 355 360 365
 Asp His Val Cys Leu Gly His Tyr
 370 375

<210> 5
 <211> 17
 <212> FRT
 <213> Homo sapiens

<400> 5
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 Ala Ala Leu Leu Gly Ala Val Ala Leu Arg Pro Ala Glu Ala Val
 20 25 30
 Ser Glu Pro Thr Thr Val Ala Phe Asp Val Arg Pro Gly Gly Val Val
 35 40 45
 His Ser Phe Ser His Asn Val Gly Pro Gly Asp Lys Tyr Thr Cys Met
 50 55 60
 Phe Thr Tyr Ala Ser Gln Gly Gly Thr Asn Glu Gln Trp Gln Met Ser
 65 70 75 80
 Leu Gly Thr Ser Glu Asp His Gln His Phe Thr Cys Thr Ile Trp Arg
 85 90 95
 Pro Gln Gly Lys Ser Tyr Leu Tyr Phe Thr Gln Phe Lys Ala Glu Val
 100 105 110
 Arg Gly Ala Glu Ile Glu Tyr Ala Met Ala Tyr Ser Lys Ala Ala Phe
 115 120 125
 Glu Arg Glu Ser Asp Val Pro Leu Lys Thr Glu Glu Phe Glu Val Thr
 130 135 140
 Lys Thr Ala Val Ala His Asp Ile Lys Ala Ile Lys Ala Ile Lys
 145 150 155
 Lys Ile Val Ala Val Lys Ala Ile Lys Ala Ile Lys Ala Ile Lys

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 <212> FRT
 <213> Homo sapiens

50 55 60
Leu Leu Arg Asp Ala Gln Gln Asn Ser
65 70

<210> /
<211> 1172
<212> FRT
<213> Homo sapiens

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20 25 30
Leu Leu Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly
35 40 45
Leu Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met
50 55 60
Lys Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His
65 70 75 80
Arg Val Glu Asn Val Ala Ser Ser Gly Pro Met Arg Trp Trp Gln
85 90 95
Ser Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg
100 105 110
Arg Phe Gln Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro Met Pro
115 120 125
Ala Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg
130 135 140
Val Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val
145 150 155 160
Arg Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu
165 170 175
Pro Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn
180 185 190
Leu Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile
195 200 205
Gln Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu
215 220 225
Ala Pro Val Pro Val Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala
230 235 240 245
Val Pro Val Leu Asn Leu Val Gly Asn Tyr Thr Tyr His Gly His Ala
250 255 260 265
Asp Arg Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala
260 265 270
Val Gln Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro
275 280 285
Asn Cys Thr Arg Cys Ala Pro Thr Tyr Asn Asn Asn Pro Thr Asn Ile
290 295 300

Gly Ala Ser Ile Gln Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp
370 375 380
Gly Ala Val Pro Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val
385 390 395 400
Cys Lys Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly
405 410 415
Phe Thr Gly Leu Thr Tyr Ala Asn Pro Gln Gly Cys His Arg Cys Asp
420 425 430
Cys Asn Ile Leu Gly Ser Arg Arg Asp Met Pro Cys Asp Glu Glu Ser
435 440 445
Gly Arg Cys Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln
450 455 460
Cys Ala Pro Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro
465 470 475 480
Cys Ala Cys Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe
485 490 495
Thr Cys Gln Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser
500 505 510
Ala Ala Ala Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala
515 520 525
Thr Gly Cys Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro
530 535 540
Gly Cys Asp Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr
545 550 555 560
Gly Pro Arg Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro
565 570 575
Val Cys Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu
580 585 590
Arg Glu Gln Ala Leu Arg Phe Gly Arg Leu Arg Asn Ala Thr Ala Ser
595 600 605
Leu Trp Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile
610 615 620
Leu Asp Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser
625 630 635 640
Pro Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu
645 650 655
Ser Leu Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu
660 665 670
Phe Gln Thr Leu Ser Leu Ile Arg Asp Leu Val Ser Leu Asp Arg Phe
675 680 685 690
Ile Arg Ile Leu Ile Thr Met Tyr Gln Asn Ile Asp Val Glu Ile Ile
700 705 710 715
Ile Ile Phe Val Ala Asp Phe Met Gly Ala Ile Asp Val Gln Asp Ile
720 725 730 735
Ala Tyr Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser
740 745 750 755
Arg Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu
760 765 770 775
Val Arg Ala Ala Gly Gly Gly Gly Thr Gly Ser Ile Lys Leu Val

520	525	530	
Gly Ile Val Ala Glu Ile Leu Arg Gly Thr Ala Ala Gln Leu Gln Arg			
"55	540	545	
Thr Arg Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln			
"58	555	560	
Ser Ser Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln			
865	870	875	880
Met Glu Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg			
"88	880	885	890
Asp Ile Leu Thr Asp Ile Asp Thr Asp Ala Ala Thr Ile Gln Glu Val			
900	905	910	
Ser Glu Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val			
915	920	925	
Leu Gln Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn			
930	935	940	
Val Asp Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg			
945	950	955	960
Arg Leu Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val			
965	970	975	
Glu Gly Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val			
980	985	990	
Ala Leu Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu			
995	1000	1005	
Arg Leu Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro			
1010	1015	1020	
Ala Glu Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp			
1025	1030	1035	1040
Thr Arg Met Glu Gln Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu			
1045	1050	1055	
Ala Val Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Gln Ala Leu			
1060	1065	1070	
Ser Ala Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu			
1075	1080	1085	
Lys Asp Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg			
1090	1095	1100	
Ile Gln Ser Val Lys Thr Glu Ala Glu Glu Ile Gly Glu Thr Met			
1105	1110	1115	1120
Glu Met Met Asp Ile Ser Lys Asp Met Gln Leu Ile Leu Leu Arg Gly			
1125	1130	1135	1140
Arg Leu Ala Ile Met Ile Asp Ile Asp Ile Asp Ile Asp Ile Asp Ile Asp			
1145	1150	1155	1160
Asp Val Ile Glu Ile Asp Asp His Ile Asp Asp Asp Val Ile Asp Val			
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Ala Thr Gys Lys			
1175			

520-1175
1110-1140

<210> 9
<211> 175
<212> PRT
<213> *Homo sapiens*

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 Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
 20 25 30
 Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
 35 40 45
 Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
 50 55 60
 Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
 65 70 75 80
 Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
 85 90 95
 Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
 100 105 110
 Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile
 115 120 125
 Met Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Thr Gly Arg
 130 135 140
 Tyr Ser Asn Ala Ile Tyr Ala Tyr Ser Pro Ala Asp Thr Ala Leu Ile
 145 150 155
 Leu Asp Asn Met Ile Lys Ala Leu Ile Ile Ile Lys Thr Ala Leu Ile
 160 165 170

<210> 10
<211> 462
<212> DNA
<213> Human Y chromosome

gtttgggggg ttcccccctca ctatcttacc ccacccggcc at

462

<210> 11

<211> 945

<212> DNA

<213> Homo sapiens

<400> 11

<210> 12

<211> 474

<212> DNA

<213> Homo sapiens

400-12

• 100 •

1970-1971

Cellular DNA

<213> *Homo sapiens*

<400> 13

at a time, and in this way, the author has been able to make a detailed study of the life and work of the author.

THE BOSTONIAN SOCIETY

221 - 519

<212> DNA

<213> *Homo sapiens*

19. 10. 1970.

<210> 15

<211> 219

(212) DNA

<213> Homo sapiens

<400 + 15

<210> 16

1. *Leucosia* *leucosia* (L.) *leucosia* (L.) *leucosia* (L.) *leucosia* (L.)

ANSWER

• 11.1.1. Handwriting

• 192 •

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<212> 1232
<213> 1177 1111.1111

• • • •

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420 JOURNAL OF CLIMATE

<210> 19

2112 1296

212 > 11MA

<213> Homo sapiens

220

220

221-663

1003-19

aag qua tao aag joo joo std got gtc att std att got act joo m111
Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala Leu
11 12 13 14 15

Arg Ser Val Cys Glu Pro Arg Glu Glu Met Arg Ile Val His Glu
100 105 110

115 Ile Phe Gly Asp Glu Leu Gly Trp Arg Val Ile Glu Ile Glu Leu Thr
120 125 130 135

acacacgacgc agttacaaaa aactccccca ggctggatgt ggtggatcac gctgtatcc 547
 ccacgacttt gggatggccaa ggtttttggat tcaatcgat tcaatgttttcc gatgttttggat 607
 tggccaaacat gatgaaaacc catatctact aaaaatcacaa aaaatttagcc gggcggtggta 717
 gggggcgcct ttagtcacag ctactcgga ggctgaggca ggagaatggc gtgaaccgg 777
 gagggggggc ttgcaatgttag ccgagatcgc gccactgcac tccagcctgg gcgacagagc 837
 gagactccgt ctcaaaaaaa aaaaaaaaaa aaaaaataca aaaatttagcc ggccgtggtg 897
 gcccacgcct gtaatccccag ctactcgga ggctaaaggca ggaattttgt ttgtacccag 957
 gaggtggagg ctgcaatgttag ctqagattgt gccacttcac tccagcctgg gtgacaaagt 1017
 gagactccgt cacaacaaca acaacaaaaa qctccccaa ctaaagccta gaagaccttc 1077
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 ttgcaggcc tttgtgtacca ggaaggaaat cagcatgtt ttagaggtaa ggatggagg 1197
 aacgtgtcac ttttaatgtt cggatgtctc aatccatcaat aggatgttac tggatccat 1257
 gaaatcgat tttttttttt aagttctcaa tgcacccat 1296

210 20

1. H_2O 2. H_2O_2 3. H_2O_3 4. H_2O_4

1.2.2.2. DNA

4213 > Homo sapiens

2200

22110 CDS

<222> (57) . . . (1001)

1000

Information about the author's current address and the offprint requests should be addressed to the author.

• 10 •

“I can’t say much for the rest of the day, but I’m sure the day will be a good one for the family.”

56

57

58

59

cca gag gag aac and gag agg att ttt gtt gat aat gta aat aat 598
 Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile Asp
 70 75 80

ggc gag aag gag gag ttt gtc act atg gat gag ctc aat gag tgg att 597
 Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Ile Lys Asp Thr Ile
 81 86 91

aaa ttt gca cca aag cgc tgg att ttt gag gat gta gag cga aat tgg 595
 Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln Trp
 100 105 110

aag ggg cat gat atc aat gag aac gtt atc ttt tgg gat gag tat 593
 Lys Gly His Asp Ile Asn Glu Asp Gly Ile Val Ser Trp Glu Ile Tyr
 115 120 125

aaa aat gcc acc tac ggc tac gtt ttt gat gat cca gat cct gat gat 491
 Lys Asn Ala Thr Tyr Gly Tyr Val Ile Asp Asp Pro Asp Pro Asp Asp
 130 135 140 145

gga ttt aac tat aaa gag atg atg gtt aya gat gag cgg agg ttt aaa 539
 Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe Lys
 150 155 160

atg gca gag aag gat gga gac ctc att gcc acc aag gag gag ttt aca 587
 Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe Thr
 165 170 175

gct ttc ctg cac cct gag gag tat gat tac atg aaa gat ata gta gta 635
 Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val Val
 180 185 190

cag gag aca atg paa paa aca paa aca aat gat ggt ttt aat paa 655
 Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile Asp
 195 200 205

ttt
 Leu
 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295

ttt
 Leu
 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380

ttt
 Leu
 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470

ttt
 Leu
 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560

ate gln gag tat gag tta ttt gtt tyc aac cag gcc aac gag ttt 571
 Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp Phe
 572 573 574 575 576 577 578 579 580 581

Arg Gln Gcc Tta Gta Cgg Cat Gtt Gag Ttt Tgaaatcagg Aaggacatcc 1021
 Gly Glu Ala Leu Val Arg His Asp Glu Ile
 319 320

<400> 21

actggagaca ctgaaggagg cagggccat tagatgtttg gttgcacaaac agatttgcag 60
atcaaggaga acccaggagt ttcaaaagaag cgttagtaag gtatctgaga tcttgcact 120
agctacatcc tcagggttgg agggaa ggt gat tcc aga aac atg cgg ctg ctc 173

Met Ala Ser Arg Ser Met Arg Leu Leu

1

5

cta ttg ctg aac tgc ctg gcc aaa aca gga gtc ctg ggt gat atc aac 221
Leu Leu Leu Ser Cys Leu Ala Lys Thr Gly Val Leu Gly Asp Ile Ile
10 15 20 25

atg aga ccc aac tgt gct cct gga tgg ttt tac cac aag tcc aat tgc 269
Met Arg Pro Ser Cys Ala Pro Gly Trp Phe Tyr His Lys Ser Asn Cys
30 35 40

tat ggt tac ttc agg aag ctg aac tgg tct gat gcc gag ctc gag 317
Tyr Gly Tyr Phe Arg Lys Leu Arg Asn Trp Ser Asp Ala Glu Leu Glu
45 50 55

tgt cag tct tac gga aac gga gcc cac ctg gca tct atc ctg agt tta 365
Cys Gln Ser Tyr Gly Asn Gly Ala His Leu Ala Ser Ile Leu Ser Leu
60 65 70

aag gaa gcc aac acc ata gca gag tac ata aat ggc tat cag aga aac 413
Lys Glu Ala Ser Thr Ile Ala Glu Tyr Ile Ser Gly Tyr Gln Arg Ser
75 80 85

u
my.

cag ccg ata tgg att ggc ctg cac gac cca cag aag agg cag cag tgg 461
Gln Pro Ile Trp Ile Gly Leu His Asp Pro Gln Lys Arg Gln Gln Trp
90 95 100 105

cag tgg att gat ggg gcc atg tat ctg tac aga tcc tgg tct ggc aag 509
Gln Trp Ile Asp Gly Ala Met Tyr Leu Tyr Arg Ser Trp Ser Gly Lys
110 115 120

tcc atg ggt ggg aac aag cac tgt gct gag atg aac tcc aat aac aac 557
Ser Met Gly Asn Lys His Cys Ala Glu Met Ser Ser Asn Asn Asn
125 130 135 140

*** The last 100 amino acids are not aligned with the sequence above
Ile Leu Ile Trp Ser Ser Asn Ala Lys Asn Lys Arg Glu His Ile Leu
145 150 155 160

tgc aag tac cga cca tagagaaatc atcaaggatcc tgcataatcc tgcacagcc 660
Cys Lys Tyr Arg Pro
155

*** Last 100 amino acids are not aligned with the sequence above

*** The last 100 amino acids are not aligned with the sequence above
Ile Leu Ile Trp Ser Ser Asn Ala Lys Asn Lys Arg Glu His Ile Leu
145 150 155 160

• 2113 • 22
• 2114 • 1148
• 2115 • 2152
• 2116 • Homo sapiens

4220
4221 CDS
4222

<221> misc features

222

623 > 1 - 8, T, C or G

1400 16

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 Val Trp Lys Val Ala Val Phe Leu Ser Val Ala Leu Gly Ile Gly Ala
 5 10 15

gtt cct ata gat gat cct gaa gat gga ggc aag cac tgg gtg gtg atc 215
 Val Pro Ile Asp Asp Pro Glu Asp Gly Gly Lys His Trp Val Val Ile
 20 25 30

gtg gca ggt tca aat ggc tgg tat aat tat agg cag cag gca gac gcg 263
 Val Ala Gly Ser Asn Gly Trp Tyr Asn Tyr Arg His Gln Ala Asp Ala
 35 40 45

tgc cat gcc tac cag atc att cac cgc tat ggg att cct gac gaa cag 311
 Cys His Ala Tyr Gln Ile Ile His Arg Asn Gly Ile Pro Asp Glu Gln
 40 45 50 55 60 65 70 75 80 85 90 95 100

ata gtt gtt atg atg tac gat gac att atc tac tat gaa gac aat aa 359
the 19th codon. Met Ile Asp Ser Lys Val Tyr Ile Ser Ile Val Ile

Thr Arg His Gly Ser Thr Gly Ile Leu Val Phe Ile Asn His Asp Leu			
134	135	161	
Met His Asp Val Asp			647
His Val Lys Asp Leu Asn Glu Thr Ile Asp Lys Tyr Lys His Lys			
165	170	175	
Met Tyr Arg Lys Met Val Phe Tyr Ile Glu Ala Cys Glu Ser Gly Ser			695
180	185	190	
Met Asp Asp Cys Val Asp Val Asp Val Asp Val Asp Val Asp Val Asp			743
Met Met Asn His Leu Pro Asp Asn Ile Asn Val Tyr Ala Thr Thr Ala			
195	200	205	
Ala Asn Asp Asp Val Asp Val Asp Val Asp Val Asp Val Asp Val Asp			781
Ala Asn Pro Arg Glu Ser Ser Tyr Ala Cys Tyr Tyr Asp Val Asp Lys Arg			
210	215	220	225
Ser Thr Tyr Leu Gly Asp Trp Tyr Ser Val Asn Trp Met Glu Asp Ser			839
230	235	240	
Asp Val Glu Asp Leu Thr Lys Glu Thr Leu His Lys Gln Tyr His Leu			887
245	250	255	
Glu Asp			935
Val Lys Ser His Thr Asn Thr His Val Met Gln Tyr Gly Asn Lys			
260	265	270	
Asp Thr Ser Thr Met Lys Val Met Gln Phe Gln Gly Met Lys Arg Lys			993
275	280	285	
Gcc Agt Tct Ccc Gtc Ccc Cta Cct Cca Gtc Aca Cac Ctt Gac Ctc Acc			1031
Ala Ser Ser Pro Val Pro Leu Pro Val Thr His Leu Asp Leu Thr			
290	295	300	305
Asp			1079
Thr Asn Asp Leu Glu Gln Ser Asp Gln Leu Thr Gln Val Ile Asn Asp			
320	325	330	335
Asp			1117
Thr Asn Asp Leu Asp Tyr Val Tyr Ala Asp Asp His Leu Tyr Val Ile Asp			

<210> 23

<211> 988

<212> DNA

<213> *Homo sapiens*

10000

<221> CDS

<222> (9), ..., (527)

400 23

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 1 5 10

tgg tgg gcc gca ctg ctc cta tgg gca gtg gca ctc ari ctc gca gac 36
 Leu Trp Ala Ala Leu Leu Gly Ala Val Ala Leu Arg Ile Ala Glu
 15 20 25 30 35

gct gtg tcc gag ccc acg acc gtg gcg ttt gac gtg cgg ccc ggc ggc 146
 Ala Val Ser Glu Pro Thr Thr Val Ala Phe Asp Val Arg Pro Gly Gly
 35 40 45

gtc gtg cat tcc tta tcc cat aac gtt; ggc cgg ttt ttt aat tat aca 174
 Val Val His Ser Phe Ser His Asp Val Gly Pro Gly Asp Lys Tyr Thr
 50 55 60 65 70 75 80

It is not clear if this is the case, but it is clear that the *hox* genes are involved in the development of the nervous system.

Very early in the day the first of the two birds left the nest, and the second followed a few hours later. The two birds were seen to fly to the same roosting place, and were heard to sing from time to time.

Val Thr Lys Thr Ala Val Ala His Arg Pro Gly Ala Thr Lys Ala Ile
116 120 124

167 Leu Ser Lys Leu Val Ile Val Ala Lys Ala Ser Arg Thr Glu Leu 168 169 170 527

<210> 24
<211> 390
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (102) ... (320)

gag ata ttt cgg atg ata atc taa atc act ttc cat gta pti atg ttt 164
 Glu Ile Phe Arg Met Ile Ile Tyr Ieu Thr Phe Pro Val Ala Met Ile
 165 166 167 168

1973 Home Showers

220
221
222

$$h_0 \frac{4}{3} \pi R^3 \rho_0 c^2 = \frac{4}{3} \pi R^3$$

Met Arg Pro Phe Phe Leu Leu

1

tgt ttt gcc ctg cct ggc ctc ctg cat gtt caa caa gcc tgc tcc agt 822
 Cys Phe Ala Leu Pro Gly Leu Leu His Ala Gln Gln Ala Cys Ser Arg
 18 19 20

10

25

25

a y

999 gac tgc tat cca cct gtt 999 gag atg ctt gtt ggg agg acc cgg 1000
 Gly Ala Cys Tyr Pro Pro Val Val Gly Asp Leu Ile Val Gly Arg Thr Arg
 25 30 35

25

30

(11)

ttt ctc aga gct tca tct acc tgg tgg acc aag ctc gag acc tar 378
 Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu Thr Lys Pro Glu Thr Tyr
 42 43 44 45 46 47 48 49 50 51 52 53 54 55

151

11

77

tgc acc cag tat ggc gag tgg cag atg aaa tgc tgc aag tgt gac tcc 966
 Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys Cys Cys Lys Cys Asp Ser
 60 61 62 63 64 65 66 67 68 69 70

60

11

2

55

11

200

140	145	150	
gtc tgc acc tcc acc ttc aat ggg gtc cgc cag gtt cgg ttt cag and			1254
Asp Cys Thr Ser Thr Phe Pro Arg Val Arg Gln Gly Arg Pro Gln Ser			
155	160	165	
ttt cag gat gtt cgg tgc cag ttt ctt ctt ctt ctt ctt ctt ctt ctt ctt			1264
Trp Gln Asp Val Arg Cys Gln Ser Leu Pro Gln Arg Pro Asn Ala Arg			
170	175	180	
ata aat ggg ggg aag gtc caa ctt aat ttg gat ttg ttg ttt ggg			1350
Leu Asn Gly Gly Lys Val Gln Leu Asn Leu Met Asp Leu Val Ser Gly			
185	190	195	
att cca gca act cca aat ctt ctt aat ctt ctt ctt ctt ctt ctt ctt ctt			1398
Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln Gln Val Gln Gln Ile Thr			
200	205	210	
aac ttg aga gtc aat ttc acc aag ctg gcc aat gtg ccc ctt aag ggc			1446
Asn Leu Arg Val Asn Phe Thr Arg Leu Ala Pro Val Pro Gln Arg Gly			
220	225	230	
ttc ccc ccc aac gtc tac tat gct gtg tcc cag ctc aat ctt ctt ctt			1494
Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val Ser Gln Leu Arg Leu Gln			
235	240	245	
ggg aac tgc ttc tgt ccc ggc ctt gat gat ccc tgc gca ccc aac aac			1542
Gly Ser Cys Phe Cys His Gly His Ala Asp Arg Cys Ala Pro Lys Pro			
250	255	260	
ggg gcc tct gca ggc ccc tcc acc gct gtg cag gtc ccc gat gtc tgt			1590
Gly Ala Ser Ala Gly Pro Ser Thr Ala Val Gln Val His Asp Val Cys			
265	270	275	
gtc tgc cag ccc aac act gcc ggc ccc aat tgt ggg cgg tgt gca ccc			1638
Val Cys Gln Asn Thr Ala Gly Pro Asn Cys Glu Arg Cys Ala Pro			
280	285	290	
ttt ttt aat aat ttt			1644
Trp Asn Asn Arg Pro Trp Asn Ile Ala Gly Val Gln Asp Ala His			
300	305	310	
ttt ttt aat aat ttt			1644
Trp Asn Asn Arg Pro Trp Asn Ile Ala Gly Val Gln Asp Ala His			
315	320	325	
ttt			1644
Trp Asn Asn Arg Pro Trp Asn Ile Ala Gly Val Gln Asp Ala His			
330	335	340	

1. The sequence of the 1644 bp fragment is identical to the sequence of the 1638 bp fragment except for the presence of a 6 bp insertion at position 1638.

tgc atc tcc tgc gag tgt gat ccc gat ggg gca gtc cca ggg gct ccc 1926
 Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly Ala Val Pro Gly Ala Pro
 380 385 390

tgt gac cca gtc acc ggg cag tgt gtc aag gag cat gtc cag gga 1974
 Cys Asp Pro Val Thr Gly Gln Cys Val Cys Lys Glu His Val Gln Gly
 395 400 405

gag cgc tgt gac cta tgc aac ccc aac ttc act cca ctc acc tac ccc 2022
 Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe Thr Gly Leu Thr Tyr Ala
 410 415 420

aac ccc cag ggc tgc ccc cgc tgt gac tgc aac atc ctc ggg tcc cgg 2070
 Asn Pro Gln Gly Cys His Arg Cys Asp Cys Asn Ile Leu Gly Ser Arg
 425 430 435

agg gac atg ccg tgt gac gag gag agt ggg cgc tgc ctt tgt ctg ccc 2118
 Arg Asp Met Pro Cys Asp Glu Glu Ser Gly Arg Cys Leu Cys Leu Pro
 440 445 450 455

aac gtg gtg ggt ccc aaa tgt gac cag tgt gct ccc tac cac tgg aag 2166
 Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala Pro Tyr His Trp Lys
 460 465 470

ctg gcc agt ggc cag ggc tgt qaa ccc tgt gcc tgc gac ccc cac aac 2214
 Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala Cys Asp Pro His Asn
 475 480 485

tcc ctc agc cca cag tgc aac cag ttc aca ggg cag tgc ccc tgt cgg 2262
 Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly Gln Cys Pro Cys Arg
 490 495 500

qaa ggc ttt ggt ggc ctg atg tgc agc gct gca gcc atc ccc cag tgt 2310
 Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala Ile Arg Gln Cys
 505 510 515

aac gac ccc acc tat gga gac ttc gtt aca gca tcc cca aac ttt ttt
 His Asp Ala Thr Tyr Gly Asp Val Ala Thr Gly Cys Arg Ala Tyr Arg
 520 525 530 535

tgc tgc tcc tgc ccc ccc ttc acc ggg ccc ccc tgc tgt gac cag tgc 2364
 Tyr Arg Ile Arg Gly Thr Val Gly Pro Arg Cys Asp Gln Cys
 540 545 550

Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln Val Ala Glu Gln Leu
 825 830 835

cgg ggc ttc aat gcc caq ctc caq cgg acc agg caj atg att agg gca 3318
 Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg Gln Met Ile Arg Ala
 840 845 850 855

gcc gag gaa tct gcc tca cag att caa tcc agt gtc cag cjc ttg gag 3366
 Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser Ala Gln Arg Leu Glu
 860 865 870

acc cag gtg agc gcc agc cgc tcc cag atg gag gaa gat gtc aga cgc 3414
 Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu Glu Asp Val Arg Arg
 875 880 885

aca cga ctc cta atc caq caq gcc egg gac ttc cta aca gac ccc gac 3462
 Thr Arg Leu Leu Ile Gln Gln Val Arg Asp Phe Leu Thr Asp Pro Asp
 890 895 900

act gat gca gcc act atc cag gag gtc agc gag gcc gtg ctg gcc ctg 3510
 Thr Asp Ala Ala Thr Ile Gln Glu Val Ser Glu Ala Val Leu Ala Leu
 905 910 915

tgg ctg ccc aca gac tca gct act gtt ctg cag aag atg aat gag atc 3558
 Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln Lys Met Asn Glu Ile
 920 925 930 935

cag gcc att gca gcc agg ctc ccc aac gtg gac ttg gtg ctg tcc cag 3606
 Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp Leu Val Ser Gln
 940 945 950

acc aag cag gac att gcg cgt gcc cgc egg ttg cag gct gag gct gag 3654
 Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu Gln Ala Glu Ala Glu
 955 960 965

gaa gcc agg agc cga gcc cat gca gtg gag ggc cag gtg gaa gat gtg 3702
 Gln Ala Arg Ser Arg Ala His Ala Val Glu Glu Gln Val Glu Asp Val
 970 975 980

acc atg caa ggc acc aqc cgc tcc ctt cgg ctt atc cag gac agg gtc 3798
 Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu Ile Gln Asp Arg Val
 1000 1005 1010 1015

ttt atp ttt
 Thr Ser
 985 990 995

acc atg caa ggc acc aqc cgc tcc ctt cgg ctt atc cag gac agg gtc 3798
 Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu Ile Gln Asp Arg Val
 1000 1005 1010 1015

ttt atp ttt
 Thr Ser
 985 990 995

Thr Arg Ile Leu Thr Val Gly Pro Glu Ser Leu Gly Ser Glu Ala Leu
60 65 70 75 80 85

gtt tcc cgg acc cgg aga gcc gct ttt aca gtt gtt ttt a** ttt a** gtt 418
 Ala Ser Pro Thr Arg Arg Ala Ala Cys Thr Val Phe Thr Ala Thr Ala
 419 420 421

95 100 105
 Ser Thr Arg Thr Trp Gly Pro Pro Leu Pro His Ser Leu Thr Gly Cys
 458

gta ttt att gag tgg ttc gtt ttc act tgt ggg ttg gag cca ttt 503
 Val Phe Ile Glu Trp Phe Val Phe Pro Cys Gly Leu Glu Pro Phe
 110 115 120

taactgttt tatacttctc aatttaaatt ttcttttaaa atttttttac tattttttgt 563
aaagcaaaca gaacccaatg cctccctttg ctcttggatg ccccaactca ggaatcatgc 623
ttgtctccct gggccatttg cggtttqgtg ggtttctgga ggytttttgtt ccattccaggc 683
tggtctccct cccttaagga gtttggtgcg cagagtggc ggtgggttgtt ctagaatggc 743
gcccggagtc cggcgtatggt gggcacagtt ctccctgcgc ctcaagttgg gggaaagaaga 803
qqqccctggg ggcctccgga gctgggttt ggccctcttc tggccatcc tatttttgt 863
tgaaggccgt gaccccagtc tgcccaactga ggggtttaggg ctggaaagca gtttatagtgt 923
tccaggcgaa agctgaggga aggaqaqaac tccctccccc gttcccaatcc aactctcggt 983
tccaaagaat ctgttttgtt gtcatttgtt ttttttgttt aactgtgtgt ggtttttttcc 1043
tcaggtgtgt gtactttgga caataaaatgg tgcgtatgact gcc 1086

<210> 27

111-966

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1.1.1. Home Page

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222 (73) ... (897)

400 27

It is the author's opinion that the best way to approach the study of the history of the United States is to study the history of the people who have lived in the United States. The author believes that the study of the history of the people who have lived in the United States is the best way to approach the study of the history of the United States.